



P1007P1D1seq1 (new)-response to 6-29-04 action.txt  
Patin DOCKET & REVIEW

## Sequence Listing

### (1) GENERAL INFORMATION:

- (i) APPLICANT: Ashkenazi, Avi J.
- (ii) TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
- (iii) NUMBER OF SEQUENCES: 28
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Genentech, Inc.
  - (B) STREET: 1 DNA Way
  - (C) CITY: South San Francisco
  - (D) STATE: California
  - (E) COUNTRY: USA
  - (F) ZIP: 94080
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: WinPatin (Genentech)
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER: US/09/993,234A
  - (B) FILING DATE: 19-NOV-2001
  - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: 08/828683
  - (B) FILING DATE: 31-MAR-1997
- (viii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: 08/625328
  - (B) FILING DATE: 1-Apr-1996
- (ix) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: 08/710802
  - (B) FILING DATE: 23-Sep-1996
- (x) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Marschang, Diane L.
  - (B) REGISTRATION NUMBER: 35,600
  - (C) REFERENCE/DOCKET NUMBER: P1007P1D1
- (xi) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: 650/225-5416
  - (B) TELEFAX: 650/952-9881

### (2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 181 amino acids
  - (B) TYPE: Amino Acid
  - (D) TOPOLOGY: Linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Gln | Arg | Pro | Arg | Gly | Cys | Ala | Ala | Val | Ala | Ala | Ala | Leu |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |
| Leu | Leu | Val | Leu | Leu | Gly | Ala | Arg | Ala | Gln | Gly | Gly | Thr | Arg | Ser |
|     |     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |
| Pro | Arg | Cys | Asp | Cys | Ala | Gly | Asp | Phe | His | Lys | Lys | Ile | Gly | Leu |
|     |     |     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |
| Phe | Cys | Cys | Arg | Gly | Cys | Pro | Ala | Gly | His | Tyr | Leu | Lys | Ala | Pro |
|     |     |     |     | 50  |     |     |     | 55  |     |     |     |     |     | 60  |
| Cys | Thr | Glu | Pro | Cys | Gly | Asn | Ser | Thr | Cys | Leu | Val | Cys | Pro | Gln |
|     |     |     |     | 65  |     |     |     | 70  |     |     |     |     |     | 75  |
| Asp | Thr | Phe | Leu | Ala | Trp | Glu | Asn | His | His | Asn | Ser | Glu | Cys | Ala |
|     |     |     |     | 80  |     |     |     | 85  |     |     |     |     |     | 90  |
| Arg | Cys | Gln | Ala | Cys | Asp | Glu | Gln | Ala | Ser | Gln | Val | Ala | Leu | Glu |
|     |     |     |     | 95  |     |     |     | 100 |     |     |     |     |     | 105 |
| Asn | Cys | Ser | Ala | Val | Ala | Asp | Thr | Arg | Cys | Gly | Cys | Lys | Pro | Gly |
|     |     |     |     | 110 |     |     |     | 115 |     |     |     |     |     | 120 |
| Trp | Phe | Val | Glu | Cys | Gln | Val | Ser | Gln | Cys | Val | Ser | Ser | Ser | Pro |
|     |     |     |     | 125 |     |     |     | 130 |     |     |     |     |     | 135 |
| Phe | Tyr | Cys | Gln | Pro | Cys | Leu | Asp | Cys | Gly | Ala | Leu | His | Arg | His |
|     |     |     |     | 140 |     |     |     | 145 |     |     |     |     |     | 150 |
| Thr | Arg | Leu | Leu | Cys | Ser | Arg | Arg | Asp | Thr | Asp | Cys | Gly | Thr | Cys |
|     |     |     |     | 155 |     |     |     | 160 |     |     |     |     |     | 165 |
| Leu | Pro | Gly | Phe | Tyr | Glu | His | Gly | Asp | Gly | Cys | Val | Ser | Cys | Pro |
|     |     |     |     | 170 |     |     |     | 175 |     |     |     |     |     | 180 |
| Thr |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

## (2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 433 base pairs
  - (B) TYPE: Nucleic Acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

### (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```

CTGCTGGGG CCCGGGCCAG NGGCAGCACT CGTAGCCCCA GGTGTGACTG 50
TGCCGGTGAC TTCCACAAGA AGATTGGTCT GTTTTGTTCAG AGAGGCTGCC 100
CAGCGGGGCA ACTACCTGAA GGCCCCTTGC ACGGAGCCCT GCGCAACTCC 150
ACCTGCCTTG TGTGTCCCCA AGACACCTTC TTGGCCTGGG AGAACCCACCA 200
TAATTCTGAA TGTGCCCGCT GCCAGGCCTG TGATGAGCAG GCCTCCAGG 250
TGGCGCTGGA GAACTGTTCA GCAGTGGCCG ACACCCGCTG TGGCTGTAAG 300
CAGGGCTGGT TTGTGGAGTG CCAGGGTCAG CCAATGTGTC AGCAGTTCA 350

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CCCTTCTAAT GCCAACCATG CCTAGACTGC GGGGCCCTGC AACGCAACAC 400

ACGGCTAATN TGTTTCCCGC AGAGATNATT GTT 433

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 base pairs  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CCCGCTGCCA GGCGCTGTGAT GAGCAGGC 28

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 base pairs  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CAGGGCCCCG CAGTCTAGGC ATGGTTGG 28

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1438 base pairs  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GAATTCCGGC GCGGAGGCCG AGAGAGAAGT CACTTGCCT GGCTCTACCT 50

TGAAGTGGTT CTCAGGGTTG GGGCGAGAGT CGGGGTGGGG ACCGAGATGC 100

AGCTCTATCC TGTGCCCTG GTCGCAGCAG GCAGCCCAGC GCTTCGCGTG 150

TTCTACTTGG CCTGTCCGCT GCCGCCTAAT GAGCTCAGGT CTAGGCCGAG 200

CAGAGGGGGC ACCTGGTCGG ACTCGGTTGG GCTCGGGCGG CCCCCCCTCC 250

CCCCGCCCGC CAGGCGGCC CTTCTCGACG GCGCGGGCGG GGCCCTGCGG 300

GCGCGGGGCT GAAGGCGGAA CCACGACGGG CAGAGAGCAC GGAGCCGGGA 350

AGCCCTGGG CGCCCGTCGG AGGGCTATGG AGCAGCGGCC GCGGGGCTGC 400

GCGGCGGTGG CGGCAGCGCT CCTCCTGGTG CTGCTGGGG CCCGGGCCA 450

GGGCGGCACT CGTAGCCCCA GGTGTGACTG TGCCGGTGAC TTCCACAAGA 500

AGATTGGTCT GTTTTGTGTC AGAGGCTGCC CAGCGGGCA CTACCTGAAG 550

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GCCCCTTGCA CGGAGCCCTG CGGCAACTCC ACCTGCCTTG TGTGTCCCCA 600  
AGACACCTTC TTGGCCTGGG AGAACACCAC TAATTCTGAA TGTGCCCGCT 650  
GCCAGGCCTG TGATGAGCAG GCCTCCCAGG TGGCGCTGGA GAACTGTTCA 700  
GCAGTGGCCG ACACCCGCTG TGGCTGTAAG CCAGGCTGGT TTGTGGAGTG 750  
CCAGGTCAGC CAATGTGTCA GCAGTTCACC CTTCTACTGC CAACCATGCC 800  
TAGACTGCGG GGCCCTGCAC CGCCACACAC GGCTACTCTG TTCCCGCAGA 850  
GATACTGACT GTGGGACCTG CCTGCCTGGC TTCTATGAAC ATGGCGATGG 900  
CTGCGTGTCC TGCCCCACGT AATTCTAGC TGTCGTGGGAG 950  
GGCGGCTGGG AGCAGAGCAG GGGCCTGGGG TGGGGCAGGT GCTGCTGGTT 1000  
CAGGAATAGG AAGAGGGGAT AGGGAGGAGG GAGCCTTGGC CCTGTGATGG 1050  
GTGGGCCCCA CTTCAGGCAA ACTTAGATGG CAAAAGAGCA ATCTGGATCC 1100  
GCCTTAGCCA GATACTAAAG GGTATTTGCC TTCACTTCA GCCAGCATT 1150  
CCCCCAGCGA TCCTAGCCAG ATATTACAGA TGATTTGTCA CTTACACAGA 1200  
GAGTCACATT GATATAGCTT TAAAACCTGG GCTGAAGGAG GTTGAGGCTG 1250  
CAGTGAGCTA TGATCGTGCC ACTGCACTTC AGCCTGGCA ACAGAGCGAG 1300  
ACCTATTAAA TAAATAAATA AATATTAAAT CTATTAAATA TTAAATATTA 1350  
AATCTATTAA ATAATAAAAT ACAAAAGGGCT GAGAGTCAGG ACTGTGCTGC 1400  
TAGTTCTCTA GGGGATCTTGG GCGAAGTGCA GAGAATT 1438

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 417 amino acids  
(B) TYPE: Amino Acid  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Gln | Arg | Pro | Arg | Gly | Cys | Ala | Ala | Val | Ala | Ala | Ala | Leu |
| 1   |     |     |     |     |     |     |     |     |     |     |     |     |     | 15  |
| Leu | Leu | Val | Leu | Leu | Gly | Ala | Arg | Ala | Gln | Gly | Gly | Thr | Arg | Ser |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     | 30  |
| Pro | Arg | Cys | Asp | Cys | Ala | Gly | Asp | Phe | His | Lys | Lys | Ile | Gly | Leu |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     | 45  |
| Phe | Cys | Cys | Arg | Gly | Cys | Pro | Ala | Gly | His | Tyr | Leu | Lys | Ala | Pro |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     | 60  |
| Cys | Thr | Glu | Pro | Cys | Gly | Asn | Ser | Thr | Cys | Leu | Val | Cys | Pro | Gln |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     | 75  |
| Asp | Thr | Phe | Leu | Ala | Trp | Glu | Asn | His | His | Asn | Ser | Glu | Cys | Ala |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     | 90  |
| 80  |     |     |     |     |     |     |     | 85  |     |     |     |     |     |     |

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Arg Cys Gln Ala Cys Asp Glu Gln Ala Ser Gln Val Ala Leu Glu  
95 100 105  
Asn Cys Ser Ala Val Ala Asp Thr Arg Cys Gly Cys Lys Pro Gly  
110 115 120  
Trp Phe Val Glu Cys Gln Val Ser Gln Cys Val Ser Ser Ser Pro  
125 130 135  
Phe Tyr Cys Gln Pro Cys Leu Asp Cys Gly Ala Leu His Arg His  
140 145 150  
Thr Arg Leu Leu Cys Ser Arg Arg Asp Thr Asp Cys Gly Thr Cys  
155 160 165  
Leu Pro Gly Phe Tyr Glu His Gly Asp Gly Cys Val Ser Cys Pro  
170 175 180  
Thr Ser Thr Leu Gly Ser Cys Pro Glu Arg Cys Ala Ala Val Cys  
185 190 195  
Gly Trp Arg Gln Met Phe Trp Val Gln Val Leu Leu Ala Gly Leu  
200 205 210  
Val Val Pro Leu Leu Leu Gly Ala Thr Leu Thr Tyr Thr Tyr Arg  
215 220 225  
His Cys Trp Pro His Lys Pro Leu Val Thr Ala Asp Glu Ala Gly  
230 235 240  
Met Glu Ala Leu Thr Pro Pro Pro Ala Thr His Leu Ser Pro Leu  
245 250 255  
Asp Ser Ala His Thr Leu Leu Ala Pro Pro Asp Ser Ser Glu Lys  
260 265 270  
Ile Cys Thr Val Gln Leu Val Gly Asn Ser Trp Thr Pro Gly Tyr  
275 280 285  
Pro Glu Thr Gln Glu Ala Leu Cys Pro Gln Val Thr Trp Ser Trp  
290 295 300  
Asp Gln Leu Pro Ser Arg Ala Leu Gly Pro Ala Ala Ala Pro Thr  
305 310 315  
Leu Ser Pro Glu Ser Pro Ala Gly Ser Pro Ala Met Met Leu Gln  
320 325 330  
Pro Gly Pro Gln Leu Tyr Asp Val Met Asp Ala Val Pro Ala Arg  
335 340 345  
Arg Trp Lys Glu Phe Val Arg Thr Leu Gly Leu Arg Glu Ala Glu  
350 355 360  
Ile Glu Ala Val Glu Val Glu Ile Gly Arg Phe Arg Asp Gln Gln  
365 370 375  
Tyr Glu Met Leu Lys Arg Trp Arg Gln Gln Gln Pro Ala Gly Leu  
380 385 390  
Gly Ala Val Tyr Ala Ala Leu Glu Arg Met Gly Leu Asp Gly Cys  
395 400 405

P1007P1D1seq1 (new)-response to 6-29-04 action.txt

Val Glu Asp Leu Arg Ser Arg Leu Gln Arg Gly Pro  
410 415

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 27 base pairs  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GGCGCTCTGG TGGCCCTTGC AGAACGCC 27

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 25 base pairs  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

TTCGGCCGAG AAGTTGAGAA ATGTC 25

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1634 base pairs  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CGGGCCCTGC GGGCGCGGGG CTGAAGGCGG AACACGACG GGCAGAGAGC 50

ACGGAGCCGG GAAGCCCCCTG GGCGCCCGTC GGAGGGCT ATG GAG 94  
Met Glu  
1

CAG CGG CCG CGG GGC TGC GCG GCG GTG GCG GCG GCG CTC 133  
Gln Arg Pro Arg Gly Cys Ala Ala Val Ala Ala Ala Leu  
5 10 15

CTC CTG GTG CTG CTG GGG GCC CGG GCC CAG GGC GGC ACT 172  
Leu Leu Val Leu Leu Gly Ala Arg Ala Gln Gly Gly Thr  
20 25

CGT AGC CCC AGG TGT GAC TGT GCC GGT GAC TTC CAC AAG 211  
Arg Ser Pro Arg Cys Asp Cys Ala Gly Asp Phe His Lys  
30 35 40

AAG ATT GGT CTG TTT TGT TGC AGA GGC TGC CCA GCG GGG 250  
Lys Ile Gly Leu Phe Cys Cys Arg Gly Cys Pro Ala Gly  
45 50

P1007P1D1seq1 (new)-response to 6-29-04 action.txt

CAC TAC CTG AAG GCC CCT TGC ACG GAG CCC TGC GGC AAC 289  
 His Tyr Leu Lys Ala Pro Cys Thr Glu Pro Cys Gly Asn  
 55 60 65

TCC ACC TGC CTT GTG TGT CCC CAA GAC ACC TTC TTG GCC 328  
 Ser Thr Cys Leu Val Cys Pro Gln Asp Thr Phe Leu Ala  
 70 75 80

TGG GAG AAC CAC CAT AAT TCT GAA TGT GCC CGC TGC CAG 367  
 Trp Glu Asn His His Asn Ser Glu Cys Ala Arg Cys Gln  
 85 90

GCC TGT GAT GAG CAG GCC TCC CAG GTG GCG CTG GAG AAC 406  
 Ala Cys Asp Glu Gln Ala Ser Gln Val Ala Leu Glu Asn  
 95 100 105

TGT TCA GCA GTG GCC GAC ACC CGC TGT GGC TGT AAG CCA 445  
 Cys Ser Ala Val Ala Asp Thr Arg Cys Gly Cys Lys Pro  
 110 115

GGC TGG TTT GTG GAG TGC CAG GTC AGC CAA TGT GTC AGC 484  
 Gly Trp Phe Val Glu Cys Gln Val Ser Gln Cys Val Ser  
 120 125 130

AGT TCA CCC TTC TAC TGC CAA CCA TGC CTA GAC TGC GGG 523  
 Ser Ser Pro Phe Tyr Cys Gln Pro Cys Leu Asp Cys Gly  
 135 140 145

GCC CTG CAC CGC CAC ACA CGG CTA CTC TGT TCC CGC AGA 562  
 Ala Leu His Arg His Thr Arg Leu Leu Cys Ser Arg Arg  
 150 155

GAT ACT GAC TGT GGG ACC TGC CTG CCT GGC TTC TAT GAA 601  
 Asp Thr Asp Cys Gly Thr Cys Leu Pro Gly Phe Tyr Glu  
 160 165 170

CAT GGC GAT GGC TGC GTG TCC TGC CCC ACG AGC ACC CTG 640  
 His Gly Asp Gly Cys Val Ser Cys Pro Thr Ser Thr Leu  
 175 180

GGG AGC TGT CCA GAG CGC TGT GCC GCT GTC TGT GGC TGG 679  
 Gly Ser Cys Pro Glu Arg Cys Ala Ala Val Cys Gly Trp  
 185 190 195

AGG CAG ATG TTC TGG GTC CAG GTG CTC CTG GCT GGC CTT 718  
 Arg Gln Met Phe Trp Val Gln Val Leu Leu Ala Gly Leu  
 200 205 210

GTG GTC CCC CTC CTG CTT GGG GCC ACC CTG ACC TAC ACA 757  
 Val Val Pro Leu Leu Gly Ala Thr Leu Thr Tyr Thr  
 215 220

TAC CGC CAC TGC TGG CCT CAC AAG CCC CTG GTT ACT GCA 796  
 Tyr Arg His Cys Trp Pro His Lys Pro Leu Val Thr Ala  
 225 230 235

GAT GAA GCT GGG ATG GAG GCT CTG ACC CCA CCA CCG GCC 835  
 Asp Glu Ala Gly Met Glu Ala Leu Thr Pro Pro Pro Ala  
 240 245

ACC CAT CTG TCA CCC TTG GAC AGC GCC CAC ACC CTT CTA 874  
 Thr His Leu Ser Pro Leu Asp Ser Ala His Thr Leu Leu  
 250 255 260

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GCA CCT CCT GAC AGC AGT GAG AAG ATC TGC ACC GTC CAG 913  
Ala Pro Pro Asp Ser Ser Glu Lys Ile Cys Thr Val Gln  
265 270 275

TTG GTG GGT AAC AGC TGG ACC CCT GGC TAC CCC GAG ACC 952  
Leu Val Gly Asn Ser Trp Thr Pro Gly Tyr Pro Glu Thr  
280 285

CAG GAG GCG CTC TGC CCG CAG GTG ACA TGG TCC TGG GAC 991  
Gln Glu Ala Leu Cys Pro Gln Val Thr Trp Ser Trp Asp  
290 295 300

CAG TTG CCC AGC AGA GCT CTT GGC CCC GCT GCT GCG CCC 1030  
Gln Leu Pro Ser Arg Ala Leu Gly Pro Ala Ala Ala Pro  
305 310

ACA CTC TCG CCA GAG TCC CCA GCC GGC TCG CCA GCC ATG 1069  
Thr Leu Ser Pro Glu Ser Pro Ala Gly Ser Pro Ala Met  
315 320 325

ATG CTG CAG CCG GGC CCG CAG CTC TAC GAC GTG ATG GAC 1108  
Met Leu Gln Pro Gly Pro Gln Leu Tyr Asp Val Met Asp  
330 335 340

GCG GTC CCA GCG CGG CGC TGG AAG GAG TTC GTG CGC ACG 1147  
Ala Val Pro Ala Arg Arg Trp Lys Glu Phe Val Arg Thr  
345 350

CTG GGG CTG CGC GAG GCA GAG ATC GAA GCC GTG GAG GTG 1186  
Leu Gly Leu Arg Glu Ala Glu Ile Glu Ala Val Glu Val  
355 360 365

GAG ATC GGC CGC TTC CGA GAC CAG CAG TAC GAG ATG CTC 1225  
Glu Ile Gly Arg Phe Arg Asp Gln Gln Tyr Glu Met Leu  
370 375

AAG CGC TGG CGC CAG CAG CAG CCC GCG GGC CTC GGA GCC 1264  
Lys Arg Trp Arg Gln Gln Pro Ala Gly Leu Gly Ala  
380 385 390

GTT TAC GCG GCC CTG GAG CGC ATG GGG CTG GAC GGC TGC 1303  
Val Tyr Ala Ala Leu Glu Arg Met Gly Leu Asp Gly Cys  
395 400 405

GTG GAA GAC TTG CGC AGC CGC CTG CAG CGC GGC CCG T 1340  
Val Glu Asp Leu Arg Ser Arg Leu Gln Arg Gly Pro  
410 415 417

GACACGGCGC CCACTTGCCA CCTAGGCGCT CTGGTGGCCC TTGCAGAAC 1390

CCTAAGTACG GTTACTTATG CGTAGACA TTTTATGTCA CTTATTAAAGC 1440

CGCTGGCACG GCCCTGCGTA GCAGCACCAG CGGGCCCCAC CCCTGCTCGC 1490

CCCTATCGCT CCAGCCAAGG CGAAGAAGCA CGAACGAATG TCGAGAGGGG 1540

GTGAAGACAT TTCTCAACTT CTCGGCCGGA GTTTGGCTGA GATCGCGTA 1590

TTAAATCTGT GAAAGAAAAC AAAAAAAA AAAAAAAA AAAA 1634

(2) INFORMATION FOR SEQ ID NO:10:

P1007P1D1seq1 (new)-response to 6-29-04 action.txt

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 29 base pairs
  - (B) TYPE: Nucleic Acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ATCAGGGACT TTCCGCTGGG GACTTTCCG 29

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 30 base pairs
  - (B) TYPE: Nucleic Acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

AGGATGGAA GTGTGTGATA TATCCTTGAT 30

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 154 amino acids
  - (B) TYPE: Amino Acid
  - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Val | Cys | Pro | Gln | Gly | Lys | Tyr | Ile | His | Pro | Gln | Asn | Asn | Ser | Ile |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |  |
| Cys | Cys | Thr | Lys | Cys | His | Lys | Gly | Thr | Tyr | Leu | Tyr | Asn | Asp | Cys |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |  |
| Pro | Gly | Pro | Gly | Gln | Asp | Thr | Asp | Cys | Arg | Glu | Cys | Glu | Ser | Gly |  |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     |     |     | 45  |  |
| Ser | Phe | Thr | Ala | Ser | Glu | Asn | His | Leu | Arg | His | Cys | Leu | Ser | Cys |  |
|     |     |     | 50  |     |     |     |     | 55  |     |     |     |     |     | 60  |  |
| Ser | Lys | Cys | Arg | Lys | Glu | Met | Gly | Gln | Val | Glu | Ile | Ser | Ser | Cys |  |
|     |     |     | 65  |     |     |     |     | 70  |     |     |     |     |     | 75  |  |
| Thr | Val | Asp | Arg | Asp | Thr | Val | Cys | Gly | Cys | Arg | Lys | Asn | Gln | Tyr |  |
|     |     |     | 80  |     |     |     |     | 85  |     |     |     |     |     | 90  |  |
| Arg | His | Tyr | Trp | Ser | Glu | Asn | Leu | Phe | Gln | Cys | Phe | Asn | Cys | Ser |  |
|     |     |     | 95  |     |     |     |     |     | 100 |     |     |     |     | 105 |  |
| Leu | Cys | Leu | Asn | Gly | Thr | Val | His | Leu | Ser | Cys | Gln | Glu | Lys | Gln |  |
|     |     |     | 110 |     |     |     |     | 115 |     |     |     |     |     | 120 |  |
| Asn | Thr | Val | Cys | Thr | Cys | His | Ala | Gly | Phe | Phe | Leu | Arg | Glu | Asn |  |
|     |     |     | 125 |     |     |     |     | 130 |     |     |     |     |     | 135 |  |
| Glu | Cys | Val | Ser | Cys | Ser | Asn | Cys | Lys | Lys | Ser | Leu | Glu | Cys | Thr |  |
|     |     |     | 140 |     |     |     |     | 145 |     |     |     |     |     | 150 |  |

P1007P1D1seq1 (new)-response to 6-29-04 action.txt  
Lys Leu Cys Leu

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 163 amino acids  
(B) TYPE: Amino Acid  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln Thr Ala Gln Met Cys  
1 5 10 15  
Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys Val Phe Cys Thr  
20 25 30  
Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp Ser Thr Tyr  
35 40 45  
Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys Gly Ser  
50 55 60  
Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg Glu  
65 70 75  
Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu  
80 85 90  
Ser Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys  
95 100 105  
Arg Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp  
110 115 120  
Val Val Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr  
125 130 135  
Ser Ser Thr Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val Val  
140 145 150  
Ala Ile Pro Gly Asn Ala Ser Arg Asp Ala Val Cys Thr  
155 160

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 170 amino acids  
(B) TYPE: Amino Acid  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Thr Cys Arg Asp Gln Glu Lys Glu Tyr Tyr Glu Pro Gln His Arg  
1 5 10 15  
Ile Cys Cys Ser Arg Cys Pro Pro Gly Thr Tyr Val Ser Ala Lys  
20 25 30  
Cys Ser Arg Ile Arg Asp Thr Val Cys Ala Thr Cys Ala Glu Asn  
35 40 45

P1007P1D1seq1 (new)-response to 6-29-04 action.txt

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Tyr | Asn | Glu | His | Trp | Asn | Tyr | Leu | Thr | Ile | Cys | Gln | Leu | Cys |
| 50  |     |     |     |     |     |     |     | 55  |     |     |     |     | 60  |     |
| Arg | Pro | Cys | Asp | Pro | Val | Met | Gly | Leu | Glu | Glu | Ile | Ala | Pro | Cys |
|     |     | 65  |     |     |     |     |     | 70  |     |     |     |     | 75  |     |
| Thr | Ser | Lys | Arg | Lys | Thr | Gln | Cys | Arg | Cys | Gln | Pro | Gly | Met | Phe |
|     |     | 80  |     |     |     | 85  |     |     |     |     |     |     | 90  |     |
| Cys | Ala | Ala | Trp | Ala | Leu | Glu | Cys | Thr | His | Cys | Glu | Leu | Leu | Ser |
|     |     |     | 95  |     |     |     |     | 100 |     |     |     |     | 105 |     |
| Asp | Cys | Pro | Pro | Gly | Thr | Glu | Ala | Glu | Leu | Lys | Asp | Glu | Val | Gly |
|     |     |     | 110 |     |     |     |     | 115 |     |     |     |     | 120 |     |
| Lys | Gly | Asn | Asn | His | Cys | Val | Pro | Cys | Lys | Ala | Gly | His | Phe | Gln |
|     |     |     | 125 |     |     |     |     | 130 |     |     |     |     | 135 |     |
| Asn | Thr | Ser | Ser | Pro | Ser | Ala | Arg | Cys | Gln | Pro | His | Thr | Arg | Cys |
|     |     |     | 140 |     |     |     |     | 145 |     |     |     |     | 150 |     |
| Glu | Asn | Gln | Gly | Leu | Val | Glu | Ala | Ala | Pro | Gly | Thr | Ala | Gln | Ser |
|     |     |     | 155 |     |     |     |     | 160 |     |     |     |     | 165 |     |
| Asp | Thr | Thr | Cys | Lys |     |     |     |     |     |     |     |     |     |     |
|     |     |     | 170 |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 119 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Leu | Glu | Gly | Leu | His | His | Asp | Gly | Gln | Phe | Cys | His | Lys | Pro |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |
| Cys | Pro | Pro | Gly | Glu | Arg | Lys | Ala | Arg | Asp | Cys | Thr | Val | Asn | Gly |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |
| Asp | Glu | Pro | Asp | Cys | Val | Pro | Cys | Gln | Glu | Gly | Lys | Glu | Tyr | Thr |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |
| Asp | Lys | Ala | His | Phe | Ser | Ser | Lys | Cys | Arg | Arg | Cys | Arg | Leu | Cys |
|     |     |     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |
| Asp | Glu | Gly | His | Gly | Leu | Glu | Val | Glu | Ile | Asn | Cys | Thr | Arg | Thr |
|     |     |     | 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |
| Gln | Asn | Thr | Lys | Cys | Arg | Cys | Lys | Pro | Asn | Phe | Phe | Cys | Asn | Ser |
|     |     |     | 80  |     |     |     |     | 85  |     |     |     |     | 90  |     |
| Thr | Val | Cys | Glu | His | Cys | Asp | Pro | Cys | Thr | Lys | Cys | Glu | His | Gly |
|     |     |     | 95  |     |     |     |     | 100 |     |     |     |     | 105 |     |
| Ile | Ile | Lys | Glu | Cys | Thr | Leu | Thr | Ser | Asn | Thr | Lys | Cys | Lys |     |
|     |     |     | 110 |     |     |     |     | 115 |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:

P1007P1D1seq1 (new)-response to 6-29-04 action.txt

- (A) LENGTH: 159 amino acids
- (B) TYPE: Amino Acid
- (C) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Ala Cys Pro Thr Gly Leu Tyr Thr His Ser Gly Glu Cys Cys Lys  
1 5 10 15

Ala Cys Asn Leu Gly Glu Gly Val Ala Gln Pro Cys Gly Ala Asn  
20 25 30

Gln Thr Val Cys Glu Pro Cys Leu Asp Ser Val Thr Phe Ser Asp  
35 40 45

Val Val Ser Ala Thr Glu Pro Cys Lys Pro Cys Thr Glu Cys Val  
50 55 60

Gly Leu Gln Ser Met Ser Ala Pro Cys Val Glu Ala Asp Asp Ala  
65 70 75

Val Cys Arg Cys Ala Tyr Gly Tyr Tyr Gln Asp Glu Thr Thr Gly  
80 85 90

Arg Cys Glu Ala Cys Arg Val Cys Glu Ala Gly Ser Gly Leu Val  
95 100 105

Phe Ser Cys Gln Asp Lys Gln Asn Thr Val Cys Glu Glu Cys Pro  
110 115 120

Asp Gly Thr Tyr Ser Asp Glu Ala Asn His Val Asp Pro Cys Leu  
125 130 135

Pro Cys Thr Val Cys Glu Asp Thr Glu Arg Gln Leu Arg Glu Cys  
140 145 150

Thr Arg Trp Ala Asp Ala Glu Cys Glu  
155

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 163 amino acids
- (B) TYPE: Amino Acid
- (C) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Ala Cys Arg Glu Lys Gln Tyr Leu Ile Asn Ser Gln Cys Cys Ser  
1 5 10 15

Leu Cys Gln Pro Gly Gln Lys Leu Val Ser Asp Cys Thr Glu Phe  
20 25 30

Thr Glu Thr Glu Cys Leu Pro Cys Gly Glu Ser Glu Phe Leu Asp  
35 40 45

Thr Trp Asn Arg Glu Thr His Cys His Gln His Lys Tyr Cys Asp  
50 55 60

Pro Asn Leu Gly Leu Arg Val Gln Gln Lys Gly Thr Ser Glu Thr  
65 70 75

P1007P1D1seq1 (new)-response to 6-29-04 action.txt

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Thr | Ile | Cys | Thr | Cys | Glu | Glu | Gly | Trp | His | Cys | Thr | Ser | Glu |
|     |     |     |     |     |     | 80  |     |     | 85  |     |     |     |     | 90  |
| Ala | Cys | Glu | Ser | Cys | Val | Leu | His | Arg | Ser | Cys | Ser | Pro | Gly | Phe |
|     |     |     |     |     |     | 95  |     |     | 100 |     |     |     |     | 105 |
| Gly | Val | Lys | Gln | Ile | Ala | Thr | Gly | Val | Ser | Asp | Thr | Ile | Cys | Glu |
|     |     |     |     | 110 |     |     |     | 115 |     |     |     |     |     | 120 |
| Pro | Cys | Pro | Val | Gly | Phe | Phe | Ser | Asn | Val | Ser | Ser | Ala | Phe | Glu |
|     |     |     |     | 125 |     |     |     | 130 |     |     |     |     |     | 135 |
| Lys | Cys | His | Pro | Trp | Thr | Ser | Cys | Glu | Thr | Lys | Asp | Leu | Val | Val |
|     |     |     |     | 140 |     |     |     | 145 |     |     |     |     |     | 150 |
| Gln | Gln | Ala | Gly | Thr | Asn | Lys | Thr | Asp | Val | Val | Cys | Gly |     |     |
|     |     |     |     | 155 |     |     |     | 160 |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 121 amino acids
  - (B) TYPE: Amino Acid
  - (C) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Cys | Pro | Glu | Arg | His | Tyr | Trp | Ala | Gln | Gly | Lys | Leu | Cys | Cys |
|     |     |     |     |     |     |     |     | 1   | 5   |     | 10  |     |     | 15  |
| Gln | Met | Cys | Glu | Pro | Gly | Thr | Phe | Leu | Val | Lys | Asp | Cys | Asp | Gln |
|     |     |     |     |     |     |     |     | 20  | 25  |     |     |     |     | 30  |
| His | Arg | Lys | Ala | Ala | Gln | Cys | Asp | Pro | Cys | Ile | Pro | Gly | Val | Ser |
|     |     |     |     |     |     |     |     | 35  | 40  |     |     |     |     | 45  |
| Phe | Ser | Pro | Asp | His | His | Thr | Arg | Pro | His | Cys | Glu | Ser | Cys | Arg |
|     |     |     |     |     |     |     |     | 50  | 55  |     |     |     |     | 60  |
| His | Cys | Asn | Ser | Gly | Leu | Leu | Val | Arg | Asn | Cys | Thr | Ile | Thr | Ala |
|     |     |     |     |     | 65  |     |     | 70  |     |     |     |     |     | 75  |
| Asn | Ala | Glu | Cys | Ala | Cys | Arg | Asn | Gly | Trp | Gln | Cys | Arg | Asp | Lys |
|     |     |     |     |     |     |     |     | 80  | 85  |     |     |     |     | 90  |
| Glu | Cys | Thr | Glu | Cys | Asp | Pro | Leu | Pro | Asn | Pro | Ser | Leu | Thr | Ala |
|     |     |     |     |     |     |     |     | 95  | 100 |     |     |     |     | 105 |
| Arg | Ser | Ser | Gln | Ala | Leu | Ser | Pro | His | Pro | Gln | Pro | Thr | His | Leu |
|     |     |     |     |     |     |     |     | 110 | 115 |     |     |     |     | 120 |

Pro

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 123 amino acids
  - (B) TYPE: Amino Acid
  - (C) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

P1007P1D1seq1 (new)-response to 6-29-04 action.txt

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Cys | His | Gly | Asn | Pro | Ser | His | Tyr | Tyr | Asp | Lys | Ala | Val | Arg |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Arg | Cys | Cys | Tyr | Arg | Cys | Pro | Met | Gly | Leu | Phe | Pro | Thr | Gln | Gln |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |
| Cys | Pro | Gln | Arg | Pro | Thr | Asp | Cys | Arg | Lys | Gln | Cys | Glu | Pro | Asp |
|     |     | 35  |     |     |     |     |     | 40  |     |     |     |     | 45  |     |
| Tyr | Tyr | Leu | Asp | Glu | Ala | Asp | Arg | Cys | Thr | Ala | Cys | Val | Thr | Cys |
|     |     |     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |
| Ser | Arg | Asp | Asp | Leu | Val | Glu | Lys | Thr | Pro | Cys | Ala | Trp | Asn | Ser |
|     |     |     | 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |
| Ser | Arg | Val | Cys | Glu | Cys | Arg | Pro | Gly | Met | Phe | Cys | Ser | Thr | Ser |
|     |     |     | 80  |     |     |     |     | 85  |     |     |     |     | 90  |     |
| Ala | Val | Asn | Ser | Cys | Ala | Arg | Cys | Phe | Phe | His | Ser | Val | Cys | Pro |
|     |     |     | 95  |     |     |     |     | 100 |     |     |     |     | 105 |     |
| Ala | Gly | Met | Ile | Val | Lys | Phe | Pro | Gly | Thr | Ala | Gln | Lys | Asn | Thr |
|     |     |     | 110 |     |     |     |     | 115 |     |     |     |     | 120 |     |
| Val | Cys | Glu |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 138 amino acids
  - (B) TYPE: Amino Acid
  - (C) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| His | Cys | Val | Gly | Asp | Thr | Tyr | Pro | Ser | Asn | Asp | Arg | Cys | Cys | His |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Glu | Cys | Arg | Pro | Gly | Asn | Gly | Met | Val | Ser | Arg | Cys | Ser | Arg | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |
| Gln | Asn | Thr | Val | Cys | Arg | Pro | Cys | Gly | Pro | Gly | Phe | Tyr | Asn | Asp |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |
| Val | Val | Ser | Ser | Lys | Pro | Cys | Lys | Pro | Cys | Thr | Trp | Cys | Asn | Leu |
|     |     |     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |
| Arg | Ser | Gly | Ser | Glu | Arg | Lys | Gln | Leu | Cys | Thr | Ala | Thr | Gln | Asp |
|     |     |     | 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |
| Thr | Val | Cys | Arg | Cys | Arg | Ala | Gly | Thr | Gln | Pro | Leu | Asp | Ser | Tyr |
|     |     |     | 80  |     |     |     |     | 85  |     |     |     |     | 90  |     |
| Lys | Pro | Gly | Val | Asp | Cys | Ala | Pro | Cys | Pro | Pro | Gly | His | Phe | Ser |
|     |     |     | 95  |     |     |     |     | 100 |     |     |     |     | 105 |     |
| Pro | Gly | Asp | Asn | Gln | Ala | Cys | Lys | Pro | Trp | Thr | Asn | Cys | Thr | Leu |
|     |     |     | 110 |     |     |     |     | 115 |     |     |     |     | 120 |     |
| Ala | Gly | Lys | His | Thr | Leu | Gln | Pro | Ala | Ser | Asn | Ser | Ser | Asp | Ala |
|     |     |     | 125 |     |     |     |     | 130 |     |     |     |     | 135 |     |

Ile Cys Glu

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 197 amino acids  
(B) TYPE: Amino Acid  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Met Gly Leu Ser Thr Val Pro Asp Leu Leu Leu Pro Leu Val Leu  
1 5 10 15

Leu Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile Gly Leu  
20 25 30

Val Pro His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys Pro  
35 40 45

Gln Gly Lys Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr  
50 55 60

Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro  
65 70 75

Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr  
80 85 90

Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser Lys Cys  
95 100 105

Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp  
110 115 120

Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr  
125 130 135

Trp Ser Glu Asn Leu Phe Gln Cys Phe Asn Cys Ser Leu Cys Leu  
140 145 150

Asn Gly Thr Val His Leu Ser Cys Gln Glu Lys Gln Asn Thr Val  
155 160 165

Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu Asn Glu Cys Val  
170 175 180

Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu Cys Thr Lys Leu Cys  
185 190 195

Leu Pro

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 167 amino acids  
(B) TYPE: Amino Acid  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

P1007P1D1seq1 (new)-response to 6-29-04 action.txt

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Gly | Ile | Trp | Thr | Leu | Leu | Pro | Leu | Val | Leu | Thr | Ser | Val |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     | 15  |     |     |
| Ala | Arg | Leu | Ser | Ser | Lys | Ser | Val | Asn | Ala | Gln | Val | Thr | Asp | Ile |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     | 30  |     |     |
| Asn | Ser | Lys | Gly | Leu | Glu | Leu | Arg | Lys | Thr | Val | Thr | Thr | Val | Glu |
|     |     |     |     | 35  |     |     |     | 40  |     |     |     | 45  |     |     |
| Thr | Gln | Asn | Leu | Glu | Gly | Leu | His | His | Asp | Gly | Gln | Phe | Cys | His |
|     |     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |
| Lys | Pro | Cys | Pro | Pro | Gly | Glu | Arg | Lys | Ala | Arg | Asp | Cys | Thr | Val |
|     |     |     |     | 65  |     |     |     | 70  |     |     |     | 75  |     |     |
| Asn | Gly | Asp | Glu | Pro | Asp | Cys | Val | Pro | Cys | Gln | Glu | Gly | Lys | Glu |
|     |     |     |     | 80  |     |     |     | 85  |     |     |     | 90  |     |     |
| Tyr | Thr | Asp | Lys | Ala | His | Phe | Ser | Ser | Lys | Cys | Arg | Arg | Cys | Arg |
|     |     |     |     | 95  |     |     |     |     | 100 |     |     |     | 105 |     |
| Leu | Cys | Asp | Glu | Gly | His | Gly | Leu | Glu | Val | Glu | Ile | Asn | Cys | Thr |
|     |     |     |     | 110 |     |     |     | 115 |     |     |     | 120 |     |     |
| Arg | Thr | Gln | Asn | Thr | Lys | Cys | Arg | Cys | Lys | Pro | Asn | Phe | Phe | Cys |
|     |     |     |     | 125 |     |     |     | 130 |     |     |     | 135 |     |     |
| Asn | Ser | Thr | Val | Cys | Glu | His | Cys | Asp | Pro | Cys | Thr | Lys | Cys | Glu |
|     |     |     |     | 140 |     |     |     | 145 |     |     |     | 150 |     |     |
| His | Gly | Ile | Ile | Lys | Glu | Cys | Thr | Leu | Thr | Ser | Asn | Thr | Lys | Cys |
|     |     |     |     | 155 |     |     |     | 160 |     |     |     | 165 |     |     |
| Lys | Glu |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 78 amino acids
- (B) TYPE: Amino Acid
- (C) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Val | Glu | Asn | Val | Pro | Pro | Leu | Arg | Trp | Lys | Glu | Phe | Val | Arg |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     | 15  |     |     |
| Arg | Leu | Gly | Leu | Ser | Asp | His | Glu | Ile | Asp | Arg | Leu | Glu | Leu | Gln |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     | 30  |     |     |
| Asn | Gly | Arg | Cys | Leu | Arg | Glu | Ala | Gln | Tyr | Ser | Met | Leu | Ala | Thr |
|     |     |     |     | 35  |     |     |     | 40  |     |     |     | 45  |     |     |
| Trp | Arg | Arg | Arg | Thr | Pro | Arg | Arg | Glu | Ala | Thr | Leu | Glu | Leu | Leu |
|     |     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |
| Gly | Arg | Val | Leu | Arg | Asp | Met | Asp | Leu | Leu | Gly | Cys | Leu | Glu | Asp |
|     |     |     |     | 65  |     |     |     | 70  |     |     |     | 75  |     |     |
| Ile | Glu | Glu |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 77 amino acids  
(B) TYPE: Amino Acid  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Ile Ala Gly Val Met Thr Leu Ser Gln Val Lys Gly Phe Val Arg  
1 5 10 15  
Lys Asn Gly Val Asn Glu Ala Lys Ile Asp Glu Ile Lys Asn Asp  
20 25 30  
Asn Val Gln Asp Thr Ala Glu Gln Lys Val Gln Leu Leu Arg Asn  
35 40 45  
Trp His Gln Leu His Gly Lys Lys Glu Ala Tyr Asp Thr Leu Ile  
50 55 60  
Lys Asp Leu Lys Lys Ala Asn Leu Cys Thr Leu Ala Glu Lys Ile  
65 70 75  
Gln Thr

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 74 amino acids  
(B) TYPE: Amino Acid  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Ile Cys Asp Asn Val Gly Lys Asp Trp Arg Arg Leu Ala Arg Gln  
1 5 10 15  
Leu Lys Val Ser Asp Thr Lys Ile Asp Ser Ile Glu Asp Arg Tyr  
20 25 30  
Pro Arg Asn Leu Thr Glu Arg Val Arg Glu Ser Leu Arg Ile Trp  
35 40 45  
Lys Asn Thr Glu Lys Glu Asn Ala Thr Val Ala His Leu Val Gly  
50 55 60  
Ala Leu Arg Ser Cys Gln Met Asn Leu Val Ala Asp Leu Val  
65 70

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 77 amino acids  
(B) TYPE: Amino Acid  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Asn Arg Pro Leu Ser Leu Lys Asp Gln Gln Thr Phe Ala Arg Ser  
1 5 10 15

P1007P1D1seq1 (new)-response to 6-29-04 action.txt  
Val Gly Leu Lys Trp Arg Lys Val Gly Arg Ser Leu Gln Arg Gly  
20 25 30

Cys Arg Ala Leu Arg Asp Pro Ala Leu Asp Ser Leu Ala Tyr Glu  
35 40 45

Tyr Glu Arg Glu Gly Leu Tyr Glu Gln Ala Phe Gln Leu Leu Arg  
50 55 60

Arg Phe Val Gln Ala Glu Gly Arg Arg Ala Thr Leu Gln Arg Leu  
65 70 75

Val Glu

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
- (B) TYPE: Amino Acid
- (C) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Ile Arg Glu Asn Leu Gly Lys His Trp Lys Asn Cys Ala Arg Lys  
1 5 10 15

Leu Gly Phe Thr Gln Ser Gln Ile Asp Glu Ile Asp His Asp Tyr  
20 25 30

Glu Arg Asp Gly Leu Lys Glu Lys Val Tyr Gln Met Leu Gln Lys  
35 40 45

Trp Val Met Arg Glu Gly Ile Lys Gly Ala Thr Val Gly Lys Leu  
50 55 60

Ala Gln Ala Leu His Gln Cys Ser Arg Ile Asp Leu Leu Ser Ser  
65 70 75

Leu Thr

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids
- (B) TYPE: Amino Acid
- (C) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Met Ala Val Ala Phe Tyr Ile Pro Asp Gln Ala Thr Leu Leu Arg  
1 5 10 15

Glu Ala Glu Gln Lys Glu Gln Gln Ile Leu Arg Leu Arg Glu Ser  
20 25 30

Gln Trp Arg Phe Leu Ala Thr Val Val Leu Glu Thr Leu Lys Gln  
35 40 45

Tyr Thr Ser Cys His Pro Lys Thr Gly Arg Lys Ser Gly Lys Tyr  
50 55 60

Arg Lys Pro

P1007P1D1seq1 (new)-response to 6-29-04 action.txt